



## SEQUENCE LISTING

<110> Gilbert, Michel  
Wakarchuk, Warren W.  
National Research Council of Canada

<120> Campylobacter Glycosyltransferases for Biosynthesis of  
Gangliosides and Ganglioside Mimics

<130> 019633-000111US

<140> US 09/816,028  
<141> 2001-03-21

<150> US 60/118,213  
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<170> PatentIn Ver. 2.1

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tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat act aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 3  
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 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase  
 Campylobacter sialyltransferase II (cstII) from C. jejuni  
 strain OH4384 (ORF 7a of lipooligosaccharide (LOS)  
 biosynthesis locus)

<400> 3

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Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	

Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys  
260 265 270  
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275 280 285  
Lys Gly Lys  
290

<210> 4  
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<220>  
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<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase  
Campylobacter sialyltransferase II (cstII) from C. jejuni  
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)  
biosynthesis locus)

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gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgc aat caa 96  
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
20 25 30  
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa ttc aaa gca gta 144  
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val  
35 40 45  
ttt tac aat cct ggt ctt ttt ttt gaa caa tac tac act tta aaa cat 192  
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
50 55 60  
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240  
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
65 70 75 80  
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288  
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
85 90 95  
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336  
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
100 105 110  
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ctc aat caa 384  
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln  
115 120 125  
aga att acc tca gga gtc tat atg tgt gca gta gct ata gcc cta gga 432  
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
130 135 140

tac	aaa	gaa	att	tat	ctt	tct	gga	att	gat	ttt	tat	caa	aat	ggg	tca	480
Tyr	Lys	Glu	Ile	Tyr	Leu	Ser	Gly	Ile	Asp	Phe	Tyr	Gln	Asn	Gly	Ser	
145					150					155					160	
tct	tat	gct	ttt	gat	acc	aaa	caa	gaa	aat	ctt	tta	aaa	ctg	gct	cct	528
Ser	Tyr	Ala	Phe	Asp	Thr	Lys	Gln	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Pro	
				165						170					175	
gat	ttt	aaa	aat	gat	cgc	tca	cac	tat	atc	gga	cat	agt	aaa	aat	aca	576
Asp	Phe	Lys	Asn	Asp	Arg	Ser	His	Tyr	Ile	Gly	His	Ser	Lys	Asn	Thr	
			180						185					190		
gat	ata	aaa	gct	tta	gaa	ttt	cta	gaa	aaa	act	tac	aaa	ata	aaa	cta	624
Asp	Ile	Lys	Ala	Leu	Glu	Phe	Leu	Glu	Lys	Thr	Tyr	Lys	Ile	Lys	Leu	
		195					200					205				
tat	tgc	tta	tgt	cct	aac	agt	ctt	tta	gca	aat	ttt	ata	gaa	cta	gcg	672
Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala	
	210					215						220				
cca	aat	tta	aat	tca	aat	ttt	atc	ata	caa	gaa	aaa	aat	aac	tac	act	720
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr	
225					230					235					240	
aaa	gat	ata	ctc	ata	cct	tct	agt	gag	gct	tat	gga	aaa	ttt	tca	aaa	768
Lys	Asp	Ile	Leu	Ile	Pro	Ser	Ser	Glu	Ala	Tyr	Gly	Lys	Phe	Ser	Lys	
				245					250						255	
aat	att	aat	ttt	aaa	aaa	ata	aaa	att	aaa	gaa	aat	att	tat	tac	aag	816
Asn	Ile	Asn	Phe	Lys	Lys	Ile	Lys	Ile	Lys	Glu	Asn	Ile	Tyr	Tyr	Lys	
			260					265						270		
ttg	ata	aaa	gat	cta	tta	aga	tta	cct	agt	gat	ata	aag	cat	tat	ttc	864
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe	
		275					280					285				
aaa	gga	aaa	taa													876
Lys	Gly	Lys														
		290														

<210> 5

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase  
Campylobacter sialyltransferase II (cstII) from C. jejuni  
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)  
biosynthesis locus)

<400> 5

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Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	
			20					25					30			
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Phe	Lys	Ala	Val	
		35					40					45				
Phe	Tyr	Asn	Pro	Gly	Leu	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	
		50				55					60					



Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn
65					70					75					80
Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr
				85					90					95	
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu
			100					105					110		
Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Leu	Asn	Gln
		115					120					125			
Arg	Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Val	Ala	Ile	Ala	Leu	Gly
	130					135					140				
Tyr	Lys	Glu	Ile	Tyr	Leu	Ser	Gly	Ile	Asp	Phe	Tyr	Gln	Asn	Gly	Ser
145					150					155					160
Ser	Tyr	Ala	Phe	Asp	Thr	Lys	Gln	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Pro
			165						170					175	
Asp	Phe	Lys	Asn	Asp	Arg	Ser	His	Tyr	Ile	Gly	His	Ser	Lys	Asn	Thr
			180					185					190		
Asp	Ile	Lys	Ala	Leu	Glu	Phe	Leu	Glu	Lys	Thr	Tyr	Lys	Ile	Lys	Leu
	195						200					205			
Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala
210					215						220				
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr
225					230					235					240
Lys	Asp	Ile	Leu	Ile	Pro	Ser	Ser	Glu	Ala	Tyr	Gly	Lys	Phe	Ser	Lys
			245						250					255	
Asn	Ile	Asn	Phe	Lys	Lys	Ile	Lys	Ile	Lys	Glu	Asn	Ile	Tyr	Tyr	Lys
		260						265					270		
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe
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Lys	Gly	Lys													
290															

<210> 6

<211> 876

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1) .. (876)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
(cstII) from C. jejuni serotype O:41

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1				5					10					15		

gat	tat	tca	aga	cta	cca	aat	gat	ttt	gat	gta	ttt	aga	tgc	aat	caa	96
Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	
			20					25					30			

ttt	tat	ttt	gaa	gat	aaa	tac	tat	ctt	ggg	aaa	aaa	tgc	aaa	gca	gta	144
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Ala	Val	
		35					40					45				

ttt	tac	aat	cct	agt	ctt	ttt	ttt	gaa	caa	tac	tac	act	tta	aaa	cat	192
Phe	Tyr	Asn	Pro	Ser	Leu	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	
	50					55					60					

tta atc caa aat caa gaa tat gag acc gaa cta atc atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
ttt aac caa gct cat cta gaa aat caa aat ttt gta aaa act ttt tac	288
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttc aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgc aca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat gga tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac gaa ata aag cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu	
195 200 205	
tat tgt tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tat act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt aca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 7  
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 <212> PRT  
 <213> Campylobacter jejuni

<220>  
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 (cstII) from C. jejuni serotype O:41

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 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln  
 20 25 30  
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val  
 35 40 45  
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
 50 55 60  
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
 65 70 75 80  
 Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr  
 85 90 95  
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
 100 105 110  
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
 115 120 125  
 Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly  
 130 135 140  
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
 145 150 155 160  
 Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro  
 165 170 175  
 Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr  
 180 185 190  
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu  
 195 200 205  
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
 210 215 220  
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
 225 230 235 240  
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys  
 245 250 255  
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys  
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 275 280 285  
 Lys Gly Lys  
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<210> 8  
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 <212> DNA  
 <213> Campylobacter jejuni

<220>  
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 <222> (1)..(876)  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:19

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gat	tat	tca	agg	cta	cca	aat	gat	ttt	gat	gta	ttt	aga	tgt	aat	caa	96
Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	
			20					25					30			
ttt	tat	ttt	gaa	gat	aaa	tac	tat	ctt	ggt	aaa	aaa	tgc	aaa	gca	gtg	144
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Ala	Val	
		35					40					45				
ttt	tac	acc	cct	aat	ttc	ttc	ttt	gag	caa	tac	tac	act	tta	aaa	cat	192
Phe	Tyr	Thr	Pro	Asn	Phe	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	
	50					55					60					
tta	atc	caa	aat	caa	gaa	tat	gag	acc	gaa	cta	att	atg	tgt	tct	aat	240
Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn	
65					70				75						80	
tac	aac	caa	gct	cat	cta	gaa	aat	gaa	aat	ttt	gta	aaa	act	ttt	tac	288
Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr	
				85				90						95		
gat	tat	ttt	cct	gat	gct	cat	ttg	gga	tat	gat	ttt	ttt	aaa	caa	ctt	336
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu	
			100					105					110			
aaa	gaa	ttt	aat	gct	tat	ttt	aaa	ttt	cac	gaa	att	tat	ttc	aat	caa	384
Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Phe	Asn	Gln	
		115					120					125				
aga	att	acc	tca	ggg	gtc	tat	atg	tgt	gca	gta	gcc	ata	gcc	cta	gga	432
Arg	Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Val	Ala	Ile	Ala	Leu	Gly	
	130					135					140					
tac	aaa	gaa	att	tat	ctt	tcg	gga	att	gat	ttt	tat	caa	aat	ggg	tca	480
Tyr	Lys	Glu	Ile	Tyr	Leu	Ser	Gly	Ile	Asp	Phe	Tyr	Gln	Asn	Gly	Ser	
145					150				155					160		
tct	tat	gct	ttt	gat	acc	aaa	caa	gaa	aat	ctt	tta	aaa	cta	gcc	cct	528
Ser	Tyr	Ala	Phe	Asp	Thr	Lys	Gln	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Pro	
			165					170						175		
gat	ttt	aaa	aat	gat	cgc	tcg	cac	tat	atc	gga	cat	agt	aaa	aat	aca	576
Asp	Phe	Lys	Asn	Asp	Arg	Ser	His	Tyr	Ile	Gly	His	Ser	Lys	Asn	Thr	
			180					185					190			
gat	ata	aaa	gct	tta	gaa	ttt	cta	gaa	aaa	act	tac	aaa	ata	aaa	cta	624
Asp	Ile	Lys	Ala	Leu	Glu	Phe	Leu	Glu	Lys	Thr	Tyr	Lys	Ile	Lys	Leu	
		195					200					205				
tat	tgc	tta	tgt	cct	aat	agt	ctt	tta	gca	aat	ttt	ata	gaa	cta	gcg	672
Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala	
	210				215						220					
cca	aat	tta	aat	tca	aat	ttt	atc	ata	caa	gaa	aaa	aat	aac	tac	act	720
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr	
225					230					235					240	

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aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
                245                250                255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
                260                265                270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
                275                280                285

aaa gga aaa taa 876
Lys Gly Lys
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<210> 9
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
      (CstII) from C. jejuni O:19

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<400> 9
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1      5      10      15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
      20      25      30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
      35      40      45
Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
      50      55      60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
      65      70      75      80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
      85      90      95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
      100      105      110
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
      115      120      125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
      130      135      140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
      145      150      155      160
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
      165      170      175
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
      180      185      190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
      195      200      205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
      210      215      220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
      225      230      235      240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
      245      250      255
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
      260      265      270

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Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
 275 280 285  
 Lys Gly Lys  
 290

<210> 10  
 <211> 294  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni strain NCTC 11168

<400> 10  
 Met Ser Met Asn Ile Asn Ala Leu Val Cys Gly Asn Gly Pro Ser Leu  
 1 5 10 15  
 Lys Asn Ile Asp Tyr Lys Arg Leu Pro Lys Gln Phe Asp Val Phe Arg  
 20 25 30  
 Cys Asn Gln Phe Tyr Phe Glu Asp Arg Tyr Phe Val Gly Lys Asp Val  
 35 40 45  
 Lys Tyr Val Phe Phe Asn Pro Phe Val Phe Phe Glu Gln Tyr Tyr Thr  
 50 55 60  
 Ser Lys Lys Leu Ile Gln Asn Glu Glu Tyr Asn Ile Glu Asn Ile Val  
 65 70 75 80  
 Cys Ser Thr Ile Asn Leu Glu Tyr Ile Asp Gly Phe Gln Phe Val Asp  
 85 90 95  
 Asn Phe Glu Leu Tyr Phe Ser Asp Ala Phe Leu Gly His Glu Ile Ile  
 100 105 110  
 Lys Lys Leu Lys Asp Phe Phe Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr  
 115 120 125  
 Asn Arg Gln Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Thr Ala Val  
 130 135 140  
 Ala Leu Gly Tyr Lys Ser Ile Tyr Ile Ser Gly Ile Asp Phe Tyr Gln  
 145 150 155 160  
 Asp Thr Asn Asn Leu Tyr Ala Phe Asp Asn Asn Lys Lys Asn Leu Leu  
 165 170 175  
 Asn Lys Cys Thr Gly Phe Lys Asn Gln Lys Phe Lys Phe Ile Asn His  
 180 185 190  
 Ser Met Ala Cys Asp Leu Gln Ala Leu Asp Tyr Leu Met Lys Arg Tyr  
 195 200 205  
 Asp Val Asn Ile Tyr Ser Leu Asn Ser Asp Glu Tyr Phe Lys Leu Ala  
 210 215 220  
 Pro Asp Ile Gly Ser Asp Phe Val Leu Ser Lys Lys Pro Lys Lys Tyr  
 225 230 235 240  
 Ile Asn Asp Ile Leu Ile Pro Asp Lys Tyr Ala Gln Glu Arg Tyr Tyr  
 245 250 255  
 Gly Lys Lys Ser Arg Leu Lys Glu Asn Leu His Tyr Lys Leu Ile Lys  
 260 265 270  
 Asp Leu Ile Arg Leu Pro Ser Asp Ile Lys His Tyr Leu Lys Glu Lys  
 275 280 285  
 Tyr Ala Asn Lys Asn Arg  
 290

<210> 11  
 <211> 873  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(873)  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:4

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<400> 11
atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
  1             5             10             15

gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa 96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
             20             25             30

ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg 144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
             35             40             45

ttt tac acc cct ggt ttc ttc ttt gag caa tac tac act tta aaa cat 192
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
             50             55             60

tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
             65             70             75             80

tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
             85             90             95

gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
             100            105            110

aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa 384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
             115            120            125

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga 432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
             130            135            140

tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca 480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
             145            150            155            160

tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct 528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
             165            170            175

gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca 576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
             180            185            190

gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta 624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
             195            200            205

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tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 12  
 <211> 291  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:4

<400> 12

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	



Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala
210					215					220					
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr
225					230					235					240
Lys	Asp	Ile	Leu	Ile	Pro	Ser	Ser	Glu	Ala	Tyr	Gly	Lys	Phe	Ser	Lys
				245					250					255	
Asn	Ile	Asn	Phe	Lys	Lys	Ile	Lys	Ile	Lys	Glu	Asn	Val	Tyr	Tyr	Lys
			260					265					270		
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe
		275					280					285			
Lys	Gly	Lys													
	290														

<210> 13  
 <211> 873  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(873)  
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
 (CstII) from C. jejuni O:36

<400> 13																
atg	aaa	aaa	ggt	att	att	gct	gga	aat	gga	cca	agt	tta	aaa	gaa	att	48
Met	Lys	Lys	Val	Ile	Ile	Ala	Gly	Asn	Gly	Pro	Ser	Leu	Lys	Glu	Ile	
1				5					10					15		
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa																96
Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	
			20					25					30			
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa aca gtg																144
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Thr	Val	
		35					40					45				
ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat																192
Phe	Tyr	Thr	Pro	Asn	Phe	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	
		50				55					60					
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat																240
Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn	
	65				70				75						80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac																288
Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr	
				85					90					95		
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt																336
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu	
			100					105					110			
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa																384
Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Phe	Asn	Gln	
		115					120					125				

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tgc gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 14

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II  
(CstII) from C. jejuni O:36

<400> 14

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	

Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val  
35 40 45  
Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His  
50 55 60  
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn  
65 70 75 80  
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr  
85 90 95  
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu  
100 105 110  
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln  
115 120 125  
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly  
130 135 140  
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser  
145 150 155 160  
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro  
165 170 175  
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr  
180 185 190  
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu  
195 200 205  
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala  
210 215 220  
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr  
225 230 235 240  
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys  
245 250 255  
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys  
260 265 270  
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe  
275 280 285  
Lys Gly Lys  
290

<210> 15  
<211> 1170  
<212> DNA  
<213> *Campylobacter jejuni*

<220>  
<223> glycosyltransferase from *C. jejuni* strain OH4384  
(ORF 4a of lipooligosaccharide (LOS) biosynthesis  
locus)

<400> 15  
atgaagaaaa taggtgtagt tataccaatc tataatgtag aaaaatattt aagagaatgt 60  
ttagatagcg ttatcaatca aacttatact aacttagaaa tcatacttgt caatgatgggt 120  
agcacagatg aacactcact caatattgca aaagaatata ccttaaaaga taaaagaata 180  
actctttttg ataagaaaaa tgggggttta agttcagcta gaaatatagg tatagaatac 240  
tttagcgggg aatataaatt aaaaaacaaa actcaacata taaaagaaaa ttctttaata 300  
gaatttcaat tggatggtta taatccttat aatatatata aagcatataa aagctctcaa 360  
gcttttaata atgaaaaaga tttaaccaat ttactttacc ctagtataga ttatattata 420  
ttcttagata gtgataatta ttggaaacta aactgcatag aagaatgcgt tataagaatg 480  
aaaaatgtgg atgtattgtg gtttgaccat gattgcacct atgaagacaa tataaaaaat 540  
aagcacaaaa aaacaaggat ggaaattttt gattttaaaa aagaatgtat aatcactcca 600  
aaagaatatg caaatcgagc attaatgtga ggatctagag atatttcttt tggatggaat 660  
ggaatgattg attttaattt tttaaagcaa attaaactta aatttataaa ttttattatc 720  
aatgaagata tacacttttg gataattttg tttgctagtg ctaataaaaat ttatgtttta 780  
tcacaaaagt tgtattttgt tcgtttaaga gcaaacagta tatcaaatca tgataagaag 840

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attacaaaag caaatgtgtc agagtatttt aaagatatat atgaaacttt cggggaaaac 900
gctaaggaag caaaaaatta tttaaaagca gcaagcaggg ttataactgc tttaaaattg 960
atagaatttt tttaaagatca aaaaaacgaa aatgcacttg ctataaaaga aacattttta 1020
ccttgctatg ccaaaaaagc tttaatgatt aaaaaattta aaaaagatcc tttaaatTTA 1080
aaggaacaat tagtttttaat taaacctttt attcaaacaa aacttcctta tgatatttgg 1140
aaatTTTtggc aaaaaataaa aaatatTTta 1170

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<210> 16
<211> 1044
<212> DNA
<213> Campylobacter jejuni

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<220>
<221> CDS
<222> (1)..(1044)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni strain OH4384 (ORF 5a
of lipooligosaccharide (LOS) biosynthesis locus)

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<400> 16
atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
1 5 10 15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
20 25 30

ata caa cga gat aaa atc gat tct tat tta cca aaa aaa act ctt gtg 144
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val
35 40 45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct 192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
50 55 60

att ata ggg gag ggg cat aaa gga tat ttt aat tat gat gaa aaa tct 240
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
65 70 75 80

aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa 288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
85 90 95

aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct 336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
100 105 110

atc caa aga ggt gtt ata gga tat aat gat tgt acc gat gga agt gaa 384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
115 120 125

gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata 432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
130 135 140

aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat 480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
145 150 155 160

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aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctt ata aaa ata gat gtg gat cat atc tat gat gct aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys	
180 185 190	
ctt tat aaa agc ttc tat ata cca aaa aac aaa tat gat gta gtt agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser	
195 200 205	
tat tca agg gtt gat att cac tat ttt aat gat aat ttt ttt ctt tgt	672
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys	
210 215 220	
aaa gat aat aat ggc aat ata ttg aaa gaa cca gga gat tgc ttg ctt	720
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu	
225 230 235 240	
atc aat aat tat aac tta aaa tgg aaa gaa gta tta att gac aga atc	768
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile	
245 250 255	
aat aac aat tgg aaa aaa gca aca aaa caa agt ttt tct tca aat ata	816
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile	
260 265 270	
cac tct tta gag caa tta aag tat aaa cac agg ata tta ttt cac act	864
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr	
275 280 285	
gaa tta aat aat tat cat ttt cct ttt tta aaa aaa cat aga gct caa	912
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln	
290 295 300	
gat att tat aaa tat aat tgg ata agt att gaa gaa ttt aaa aaa ttc	960
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe	
305 310 315 320	
tat tta caa aat att aat cat aaa ata gaa cct tct atg att tca aaa	1008
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys	
325 330 335	
gaa act cta aaa aaa ata ttc tta aca ttg ttt taa	1044
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe	
340 345	

<210> 17  
 <211> 347  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni strain OH4384 (ORF 5a  
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 17

Met	Leu	Phe	Gln	Ser	Tyr	Phe	Val	Lys	Ile	Ile	Cys	Leu	Phe	Ile	Pro
1				5					10					15	
Phe	Arg	Lys	Ile	Arg	His	Lys	Ile	Lys	Lys	Thr	Phe	Leu	Leu	Lys	Asn
			20					25					30		
Ile	Gln	Arg	Asp	Lys	Ile	Asp	Ser	Tyr	Leu	Pro	Lys	Lys	Thr	Leu	Val
		35				40						45			
Gln	Ile	Asn	Lys	Tyr	Asn	Asn	Glu	Asp	Leu	Ile	Lys	Leu	Asn	Lys	Ala
	50					55					60				
Ile	Ile	Gly	Glu	Gly	His	Lys	Gly	Tyr	Phe	Asn	Tyr	Asp	Glu	Lys	Ser
65					70					75					80
Lys	Asp	Pro	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Ala	Phe	Ile	Arg	Val	Lys
				85					90					95	
Asn	Glu	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala
			100					105					110		
Ile	Gln	Arg	Gly	Val	Ile	Gly	Tyr	Asn	Asp	Cys	Thr	Asp	Gly	Ser	Glu
		115					120					125			
Glu	Ile	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Ser	Phe	Ile	Pro	Ile
	130					135					140				
Lys	Tyr	Pro	Tyr	Glu	Ile	Gln	Ile	Gln	Asn	Pro	Lys	Ser	Glu	Glu	Asn
145					150					155					160
Lys	Leu	Tyr	Ser	Tyr	Asn	Tyr	Val	Ala	Ser	Phe	Ile	Pro	Lys	Asp	
				165				170						175	
Glu	Trp	Leu	Ile	Lys	Ile	Asp	Val	Asp	His	Ile	Tyr	Asp	Ala	Lys	Lys
			180				185						190		
Leu	Tyr	Lys	Ser	Phe	Tyr	Ile	Pro	Lys	Asn	Lys	Tyr	Asp	Val	Val	Ser
		195					200					205			
Tyr	Ser	Arg	Val	Asp	Ile	His	Tyr	Phe	Asn	Asp	Asn	Phe	Phe	Leu	Cys
	210				215						220				
Lys	Asp	Asn	Asn	Gly	Asn	Ile	Leu	Lys	Glu	Pro	Gly	Asp	Cys	Leu	Leu
225					230					235					240
Ile	Asn	Asn	Tyr	Asn	Leu	Lys	Trp	Lys	Glu	Val	Leu	Ile	Asp	Arg	Ile
				245					250					255	
Asn	Asn	Asn	Trp	Lys	Lys	Ala	Thr	Lys	Gln	Ser	Phe	Ser	Ser	Asn	Ile
			260				265						270		
His	Ser	Leu	Glu	Gln	Leu	Lys	Tyr	Lys	His	Arg	Ile	Leu	Phe	His	Thr
		275					280					285			
Glu	Leu	Asn	Asn	Tyr	His	Phe	Pro	Phe	Leu	Lys	Lys	His	Arg	Ala	Gln
	290				295						300				
Asp	Ile	Tyr	Lys	Tyr	Asn	Trp	Ile	Ser	Ile	Glu	Glu	Phe	Lys	Lys	Phe
305					310					315					320
Tyr	Leu	Gln	Asn	Ile	Asn	His	Lys	Ile	Glu	Pro	Ser	Met	Ile	Ser	Lys
			325						330					335	
Glu	Thr	Leu	Lys	Lys	Ile	Phe	Leu	Thr	Leu	Phe					
			340					345							

<210> 18

<211> 1608

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1) .. (1608)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:1

<400> 18

atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att	48
Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile	
1 5 10 15	
gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa	96
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys	
20 25 30	
aaa atc tac aat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac	144
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn	
35 40 45	
tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	

att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	
aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	



aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta	1488
Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu	
485 490 495	
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata	1536
Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile	
500 505 510	
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa	1584
Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys	
515 520 525	
aga gtt aat aat ata agc ttc tta	1608
Arg Val Asn Asn Ile Ser Phe Leu	
530 535	

<210> 19

<211> 536

<212> PRT

<213> Campylobacter jejuni

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:1

<400> 19

Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile	
1 5 10 15	
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys	
20 25 30	
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn	
35 40 45	
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	

Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg  
 275 280 285  
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg  
 290 295 300  
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala  
 305 310 315 320  
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu  
 325 330 335  
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala  
 340 345 350  
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp  
 355 360 365  
 Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg  
 370 375 380  
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu  
 385 390 395 400  
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln  
 405 410 415  
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu  
 420 425 430  
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys  
 435 440 445  
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys  
 450 455 460  
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro  
 465 470 475 480  
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu  
 485 490 495  
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile  
 500 505 510  
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys  
 515 520 525  
 Arg Val Asn Asn Ile Ser Phe Leu  
 530 535

<210> 20  
 <211> 1056  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(1056)  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni O:10

<400> 20  
 atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48  
 Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro  
 1 5 10 15  
  
 ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96  
 Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn  
 20 25 30  
  
 ata caa cga gat aaa atc gat tct tat cta cca aaa aaa act ctt ata 144  
 Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile  
 35 40 45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct	192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
att ata ggg ggg ggg cat aaa gga tat ttt aat tat gat gaa aaa tct	240
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa	288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct	336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
att caa aga ggt gtt ata gga tat aat gat tgc acc gat gga agt gaa	384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata	432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat	480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctc ata aaa ata gat gtg gat cat tat tat gat gca aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
tta tat aag agt ttt tat ata cct aga aaa aat tat cat gta att agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
tac tct agg ata gat ttt ata ttt aat gaa gaa aaa ttt tat gtt tat	672
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
cgg aat aag gag ggg gag att tta aaa gct cct gga gat tgt tta gca	720
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
ata caa aac act aac tta ttt tgg aaa gaa ata ctt att gaa gat gat	768
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
aca ttt aag tgg aat act gca aaa aat aat ata gag aat gca aaa tca	816
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	
tat gaa att tta aaa gtt aga aat aga att tat ttt act aca gaa ctt	864
Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu	
275 280 285	

aat aat tat cat ttt cca ttt ata aaa aat tat aga aaa aat gat tat	912
Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr	
290 295 300	
aag cag tta aat tgg gtt agc tta gat gat ttt att aaa aat tat aaa	960
Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys	
305 310 315 320	
gaa aaa tta aaa aat caa ata gat ttt aaa atg cta gaa tac aaa aca	1008
Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr	
325 330 335	
tta aaa aaa gtg tac aaa aag ctt aca tct tca gca agc gat aaa att	1056
Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile	
340 345 350	

<210> 21  
 <211> 352  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni O:10

<400> 21

Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro	
1 5 10 15	
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn	
20 25 30	
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile	
35 40 45	
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	

Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu  
                   275                                  280                                  285  
 Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr  
                   290                                  295                                  300  
 Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys  
 305                                  310                                  315                                  320  
 Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr  
                                   325                                  330                                  335  
 Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile  
                   340                                  345                                  350

<210> 22  
 <211> 945  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(945)  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
           transferase from C. jejuni O:36

<400> 22  
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 Met Leu Lys Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys  
   1                                  5                                  10                                  15  
  
 aaa ttg gtt tta gat aat gag cat ttc att aag gaa aat aaa aac atc 96  
 Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile  
                                   20                                  25                                  30  
  
 tat gga aaa aaa cat aag ggc ttt ttt gac ttt gat gaa aag gct aag 144  
 Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys  
                                   35                                  40                                  45  
  
 gat gtg aaa tca ccc ctt aat cct tgg gga ttt atc agg gtt aaa aat 192  
 Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn  
   50                                  55                                  60  
  
 gaa gct tta acc cta aga gtt tct tta gaa agt ata cta cct gct tta 240  
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu  
   65                                  70                                  75                                  80  
  
 caa aga gga att ata gct tac aac gac tgt gat gat ggg agt gaa gag 288  
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu  
                                   85                                  90                                  95  
  
 ctt att tta gaa ttt tgc aag caa tat ccc aac ttc att gct aaa aaa 336  
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys  
                                   100                                  105                                  110  
  
 tat cct tat aaa gta gat cta gaa aat cct aaa aat gaa gaa aat aaa 384  
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys  
                                   115                                  120                                  125  
  
 ctt tac tct tat tac aat tgg gca gca tct ttt ata ccc tta gat gag 432  
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu  
   130                                  135                                  140

tgg ttt ata aaa atc gat gtg gat cat tac tac gat gcc aag aag ctt	480
Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu	
145 150 155 160	
tat aag agt ttt tat agg att gat caa gaa aat aaa gcc tta tgc tac	528
Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr	
165 170 175	
cca aga att aat ttt ata atc tta aat gga aat att tat gtg caa aat	576
Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn	
180 185 190	
agt gga aat tat gga ttc ata ggg ggg ggg gat caa ctc ttg att aaa	624
Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys	
195 200 205	
aga aga aat agt agc ttt ata gaa aga agg gtt tca aaa aaa agc caa	672
Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln	
210 215 220	
tgg ata gat cct aag gga ctt ata gaa gaa ctc tac tcc gag caa caa	720
Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
gtc tta tct caa gga gtg aaa ata cta caa gct ccc cta ctt cag tgg	768
Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp	
245 250 255	
cat ttt cct gcc tta aaa tac cgc cga aac gat tac caa caa tat tta	816
His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu	
260 265 270	
gat atc ttg agt tta gaa gaa ttt cag gcc ttt cat cgt aag agc aaa	864
Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys	
275 280 285	
gag gct aaa aaa ata gac ttt gcc atg cta aaa cgc cct gta atc gag	912
Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu	
290 295 300	
caa ata tta aag aaa ttt caa gga gag ata aaa	945
Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys	
305 310 315	

<210> 23

<211> 315

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
transferase from C. jejuni O:36

<400> 23

Met Leu Lys Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys	
1 5 10 15	
Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile	
20 25 30	
Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys	
35 40 45	

Asp	Val	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Gly	Phe	Ile	Arg	Val	Lys	Asn
50						55					60				
Glu	Ala	Leu	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala	Leu
65					70					75					80
Gln	Arg	Gly	Ile	Ile	Ala	Tyr	Asn	Asp	Cys	Asp	Asp	Gly	Ser	Glu	Glu
				85					90					95	
Leu	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Asn	Phe	Ile	Ala	Lys	Lys
			100					105					110		
Tyr	Pro	Tyr	Lys	Val	Asp	Leu	Glu	Asn	Pro	Lys	Asn	Glu	Glu	Asn	Lys
	115						120					125			
Leu	Tyr	Ser	Tyr	Tyr	Asn	Trp	Ala	Ala	Ser	Phe	Ile	Pro	Leu	Asp	Glu
	130					135					140				
Trp	Phe	Ile	Lys	Ile	Asp	Val	Asp	His	Tyr	Tyr	Asp	Ala	Lys	Lys	Leu
145				150						155					160
Tyr	Lys	Ser	Phe	Tyr	Arg	Ile	Asp	Gln	Glu	Asn	Lys	Ala	Leu	Cys	Tyr
			165					170						175	
Pro	Arg	Ile	Asn	Phe	Ile	Ile	Leu	Asn	Gly	Asn	Ile	Tyr	Val	Gln	Asn
			180					185					190		
Ser	Gly	Asn	Tyr	Gly	Phe	Ile	Gly	Gly	Gly	Asp	Gln	Leu	Leu	Ile	Lys
	195						200					205			
Arg	Arg	Asn	Ser	Ser	Phe	Ile	Glu	Arg	Arg	Val	Ser	Lys	Lys	Ser	Gln
	210					215					220				
Trp	Ile	Asp	Pro	Lys	Gly	Leu	Ile	Glu	Glu	Leu	Tyr	Ser	Glu	Gln	Gln
225					230					235					240
Val	Leu	Ser	Gln	Gly	Val	Lys	Ile	Leu	Gln	Ala	Pro	Leu	Leu	Gln	Trp
			245						250					255	
His	Phe	Pro	Ala	Leu	Lys	Tyr	Arg	Arg	Asn	Asp	Tyr	Gln	Gln	Tyr	Leu
			260					265					270		
Asp	Ile	Leu	Ser	Leu	Glu	Glu	Phe	Gln	Ala	Phe	His	Arg	Lys	Ser	Lys
	275						280					285			
Glu	Ala	Lys	Lys	Ile	Asp	Phe	Ala	Met	Leu	Lys	Arg	Pro	Val	Ile	Glu
	290					295					300				
Gln	Ile	Leu	Lys	Lys	Phe	Gln	Gly	Glu	Ile	Lys					
305					310					315					

<210> 24  
 <211> 1608  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(1608)  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni NCTC 11168

<400> 24																	
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Met	Thr	Leu	Phe	Tyr	Lys	Ile	Ile	Ala	Phe	Leu	Arg	Leu	Leu	Lys	Ile		
1				5					10					15			
gat	aaa	aaa	tta	aaa	ttt	gat	aat	gaa	tat	ttt	tta	aac	tta	aat	aaa		96
Asp	Lys	Lys	Leu	Lys	Phe	Asp	Asn	Glu	Tyr	Phe	Leu	Asn	Leu	Asn	Lys		
			20					25					30				
aaa	atc	tac	gat	gaa	aag	cat	aaa	ggg	ttt	ttt	gat	ttt	gat	cca	aac		144
Lys	Ile	Tyr	Asp	Glu	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Pro	Asn		
		35					40					45					

tca	aaa	gat	aca	aaa	tct	cct	tta	aat	cca	tgg	gct	ttt	ata	aga	gta	192
Ser	Lys	Asp	Thr	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Ala	Phe	Ile	Arg	Val	
	50					55					60					
aaa	aat	gaa	gcc	act	act	tta	aga	gta	tca	ctt	gaa	agt	atg	tta	cct	240
Lys	Asn	Glu	Ala	Thr	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Met	Leu	Pro	
	65				70					75					80	
gcc	ata	caa	aga	ggg	gtt	ata	gga	tat	aat	gat	tgt	act	gat	gga	agt	288
Ala	Ile	Gln	Arg	Gly	Val	Ile	Gly	Tyr	Asn	Asp	Cys	Thr	Asp	Gly	Ser	
				85					90					95		
gaa	gaa	att	att	ttg	gaa	ttt	tgc	aaa	caa	tac	cct	tcg	ttt	ata	cca	336
Glu	Glu	Ile	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Ser	Phe	Ile	Pro	
			100					105					110			
gta	aaa	tat	ccc	cat	gag	gtg	caa	att	gaa	aat	ccg	caa	agc	gaa	gaa	384
Val	Lys	Tyr	Pro	His	Glu	Val	Gln	Ile	Glu	Asn	Pro	Gln	Ser	Glu	Glu	
		115					120					125				
aat	aaa	ctt	cat	agt	tat	tat	aac	tat	gta	gct	agt	ttt	ata	ccg	caa	432
Asn	Lys	Leu	His	Ser	Tyr	Tyr	Asn	Tyr	Val	Ala	Ser	Phe	Ile	Pro	Gln	
	130					135					140					
gat	gag	tgg	ctt	ata	aaa	ata	gat	gtg	gat	cat	tac	tat	gat	gca	aaa	480
Asp	Glu	Trp	Leu	Ile	Lys	Ile	Asp	Val	Asp	His	Tyr	Tyr	Asp	Ala	Lys	
	145				150					155					160	
aaa	tta	tat	aag	agt	ttt	tat	atg	gca	tca	aaa	aat	act	gct	gtt	aga	528
Lys	Leu	Tyr	Lys	Ser	Phe	Tyr	Met	Ala	Ser	Lys	Asn	Thr	Ala	Val	Arg	
				165					170					175		
ttt	cca	aga	att	aat	ttt	tta	ata	cta	gat	aaa	att	gta	att	caa	aat	576
Phe	Pro	Arg	Ile	Asn	Phe	Leu	Ile	Leu	Asp	Lys	Ile	Val	Ile	Gln	Asn	
			180					185					190			
ata	gga	gaa	tgt	ggg	ttt	atc	gat	gga	ggg	gat	caa	ttg	tta	att	caa	624
Ile	Gly	Glu	Cys	Gly	Phe	Ile	Asp	Gly	Gly	Asp	Gln	Leu	Leu	Ile	Gln	
		195					200					205				
aag	tgc	aat	agt	gta	ttt	ata	gaa	aga	atg	gtt	tca	aag	caa	agt	cag	672
Lys	Cys	Asn	Ser	Val	Phe	Ile	Glu	Arg	Met	Val	Ser	Lys	Gln	Ser	Gln	
	210					215					220					
tgg	att	gat	cct	gaa	aaa	act	gtg	aaa	gaa	ttg	tat	tct	gaa	cag	caa	720
Trp	Ile	Asp	Pro	Glu	Lys	Thr	Val	Lys	Glu	Leu	Tyr	Ser	Glu	Gln	Gln	
	225				230					235					240	
att	ata	ccc	aaa	cat	ata	aaa	atc	tta	caa	gca	gaa	tta	ctt	caa	tgg	768
Ile	Ile	Pro	Lys	His	Ile	Lys	Ile	Leu	Gln	Ala	Glu	Leu	Leu	Gln	Trp	
				245					250					255		
cat	ttt	cct	gct	tta	aaa	tat	cat	aga	aat	gat	tat	caa	aaa	cat	ttg	816
His	Phe	Pro	Ala	Leu	Lys	Tyr	His	Arg	Asn	Asp	Tyr	Gln	Lys	His	Leu	
			260					265					270			
gat	gct	tta	act	tta	gaa	gat	ttt	aaa	aaa	atc	cat	tat	aga	cat	aga	864
Asp	Ala	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Lys	Ile	His	Tyr	Arg	His	Arg	
		275					280					285				



aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	
aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta	1488
Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu	
485 490 495	
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata	1536
Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile	
500 505 510	
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa	1584
Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys	
515 520 525	

aga gtt aat aat ata agc ttc tta  
 Arg Val Asn Asn Ile Ser Phe Leu  
 530 535

1608

<210> 25  
 <211> 536  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)  
 transferase from C. jejuni NCTC 11168

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 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile  
 1 5 10 15  
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys  
 20 25 30  
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn  
 35 40 45  
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val  
 50 55 60  
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro  
 65 70 75 80  
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser  
 85 90 95  
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro  
 100 105 110  
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu  
 115 120 125  
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln  
 130 135 140  
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys  
 145 150 155 160  
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg  
 165 170 175  
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn  
 180 185 190  
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln  
 195 200 205  
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln  
 210 215 220  
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln  
 225 230 235 240  
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp  
 245 250 255  
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu  
 260 265 270  
 Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg  
 275 280 285  
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg  
 290 295 300  
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala  
 305 310 315 320  
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu  
 325 330 335  
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala  
 340 345 350  
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp  
 355 360 365



cta aat gct tgt gaa gag tgt ata aaa att tta gat gaa cag gat gaa	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu	
100 105 110	
gtt gat tta gtg ttt ttc aat gct att gtt gaa agt aat gtt att tca	384
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser	
115 120 125	
tat aaa aag ttt gac ttt aat tct ggt ttt tat agc aaa aaa gag ttt	432
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe	
130 135 140	
gta aaa aaa att att gca aag aaa aat tta tat tgg act atg tgg ggg	480
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly	
145 150 155 160	
aaa ctt ata aga aag aaa ttg tat tta gaa gct ttt gcg agt tta aga	528
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg	
165 170 175	
ctc gag aaa gat gtt aaa atc aat atg gct gaa gat gta ttg tta tat	576
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr	
180 185 190	
tat cca atg tta agt caa gct caa aaa ata gca tat atg aac tgt aat	624
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn	
195 200 205	
tta tat cat tac gtg cct aat aat aat tca att tgt aat act aag aat	672
Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn	
210 215 220	
gaa gtg ctt gtt aaa aat aat att caa gag ttg cag ttg gtt tta aac	720
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn	
225 230 235 240	
tat tta agg caa aat tat att tta aac aag tat tgt agc gtt ctc tat	768
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr	
245 250 255	
gtg cta att aaa tat ttg cta tat att caa ata tat aaa ata aaa aga	816
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg	
260 265 270	
aca aaa tta atg gtt aca tta tta gct aaa ata aat att tta act tta	864
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu	
275 280 285	
aaa att tta ttt aaa tat aaa aaa ttt tta aaa caa tgt taa	906
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys	
290 295 300	

<210> 27

<211> 301

<212> PRT

<213> Campylobacter jejuni

<220>  
 <223> beta-1,3-galactosyltransferase from *C. jejuni* strain  
 OH4384 (ORF 6a of lipooligosaccharide (LOS)  
 biosynthesis locus)

<400> 27  
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 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile  
 20 25 30  
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile  
 35 40 45  
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn  
 50 55 60  
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val  
 65 70 75 80  
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu  
 85 90 95  
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu  
 100 105 110  
 Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser  
 115 120 125  
 Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe  
 130 135 140  
 Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly  
 145 150 155 160  
 Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg  
 165 170 175  
 Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr  
 180 185 190  
 Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn  
 195 200 205  
 Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn  
 210 215 220  
 Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn  
 225 230 235 240  
 Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr  
 245 250 255  
 Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg  
 260 265 270  
 Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu  
 275 280 285  
 Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys  
 290 295 300

<210> 28  
 <211> 912  
 <212> DNA  
 <213> *Campylobacter jejuni*

<220>  
 <221> CDS  
 <222> (1)..(912)  
 <223> *Campylobacter glycosyltransferase B (CgtB)* beta-1,3  
 galactosyltransferase from *C. jejuni* serotype O:2  
 (strain NCTC 11168)

<400> 28

atg agt caa att tcc atc ata cta cca act tat aat gtg gaa aaa tat	48
Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr	
1 5 10 15	
att gct aga gca tta gaa agt tgc att aac caa act ttt aaa gat ata	96
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile	
20 25 30	
gaa atc att gta gta gat gat tgt ggt aat gat aaa agt ata gat ata	144
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile	
35 40 45	
gct aaa gag tat gct agt aaa gat gat aga ata aaa atc ata cat aat	192
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn	
50 55 60	
gaa gag aat tta aag ctt tta aga gca aga tat gaa ggt gct aaa gta	240
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val	
65 70 75 80	
gca act tca cct tat atc atg ttt tta gat tct gat gat tat tta gaa	288
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu	
85 90 95	
ctt aat gct tgc gaa gaa tgt att aaa att ttg gat atg ggt ggg ggg	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly	
100 105 110	
ggt aaa att gat ttg ttg tgt ttt gaa gct ttt att acc aat gca aaa	384
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys	
115 120 125	
aaa tca ata aaa aaa tta aat ata aaa caa gga aaa tac aac aac aaa	432
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys	
130 135 140	
gaa ttt aca atg caa ata ctt aaa act aaa aat cca ttt tgg aca atg	480
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met	
145 150 155 160	
tgg gct aaa ata atc aaa aaa gat att tat tta aaa gcc ttc aac atg	528
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met	
165 170 175	
tta aat ctc aaa aaa gaa atc aaa ata aat atg gca gaa gat gcc tta	576
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu	
180 185 190	
tta tat tat cct ttg aca ata tta tct aat gaa ata ttt tac tta aca	624
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr	
195 200 205	
caa cct ttg tat acc cag cat gta aat agc aat tct ata aca aat aat	672
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn	
210 215 220	
att aat tct tta gaa gct aat att caa gaa cat aaa att gtt tta aat	720
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn	
225 230 235 240	

gtt tta aaa tca att aaa aat aaa aaa aca cct cta tat ttt cta att	768
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile	
245 250 255	
ata tat tta tta aaa att caa tta ttg aaa tat gaa caa aat ttt aat	816
Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn	
260 265 270	
aaa aga aat ata aat ctt att tat tat aaa ata aat att tta tat caa	864
Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln	
275 280 285	
aaa tat caa ttc aaa tgg aaa aaa ttt tta tat aat tta att ccg taa	912
Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro	
290 295 300	

<210> 29  
 <211> 303  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter glycosyltransferase B (CgtB) beta-1,3  
 galactosyltransferase from C. jejuni serotype O:2  
 (strain NCTC 11168)

<400> 29

Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr	
1 5 10 15	
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile	
20 25 30	
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile	
35 40 45	
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn	
50 55 60	
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val	
65 70 75 80	
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu	
85 90 95	
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly	
100 105 110	
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys	
115 120 125	
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys	
130 135 140	
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met	
145 150 155 160	
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met	
165 170 175	
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu	
180 185 190	
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr	
195 200 205	
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn	
210 215 220	
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn	
225 230 235 240	
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile	
245 250 255	

Ile	Tyr	Leu	Leu	Lys	Ile	Gln	Leu	Leu	Lys	Tyr	Glu	Gln	Asn	Phe	Asn
		260					265						270		
Lys	Arg	Asn	Ile	Asn	Leu	Ile	Tyr	Tyr	Lys	Ile	Asn	Ile	Leu	Tyr	Gln
		275					280					285			
Lys	Tyr	Gln	Phe	Lys	Trp	Lys	Lys	Phe	Leu	Tyr	Asn	Leu	Ile	Pro	
	290					295					300				

<210> 30  
 <211> 891  
 <212> DNA  
 <213> Campylobacter jejuni

<220>  
 <221> CDS  
 <222> (1)..(891)  
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 30																
atg	ttt	aaa	att	tca	atc	atc	ttg	cca	act	tat	aat	gtg	gaa	caa	tat	48
Met	Phe	Lys	Ile	Ser	Ile	Ile	Leu	Pro	Thr	Tyr	Asn	Val	Glu	Gln	Tyr	
1				5				10					15			
ata	gca	agg	gca	ata	gaa	agt	tgt	atc	aat	cag	act	ttt	aaa	aat	ata	96
Ile	Ala	Arg	Ala	Ile	Glu	Ser	Cys	Ile	Asn	Gln	Thr	Phe	Lys	Asn	Ile	
			20				25						30			
gaa	ata	att	gta	gtt	gat	gat	tgt	gga	agt	gac	aaa	agt	ata	gat	ata	144
Glu	Ile	Ile	Val	Val	Asp	Asp	Cys	Gly	Ser	Asp	Lys	Ser	Ile	Asp	Ile	
		35				40						45				
gtt	aaa	gaa	tat	gcc	aaa	aaa	gat	gat	aga	ata	aaa	atc	ata	cat	aat	192
Val	Lys	Glu	Tyr	Ala	Lys	Lys	Asp	Asp	Arg	Ile	Lys	Ile	Ile	His	Asn	
	50					55					60					
gaa	gaa	aat	tta	aaa	ctt	tta	aga	gct	aga	tat	gaa	ggt	gta	aaa	gta	240
Glu	Glu	Asn	Leu	Lys	Leu	Leu	Arg	Ala	Arg	Tyr	Glu	Gly	Val	Lys	Val	
65					70				75					80		
gca	aac	tct	cct	tat	ata	atg	ttt	tta	gat	cct	gat	gat	tat	tta	gaa	288
Ala	Asn	Ser	Pro	Tyr	Ile	Met	Phe	Leu	Asp	Pro	Asp	Asp	Tyr	Leu	Glu	
			85					90						95		
ctt	aat	gct	tgt	gaa	gaa	tgt	atg	aaa	att	tta	aaa	aac	aat	gaa	ata	336
Leu	Asn	Ala	Cys	Glu	Glu	Cys	Met	Lys	Ile	Leu	Lys	Asn	Asn	Glu	Ile	
			100					105					110			
gat	tta	tta	ttt	ttt	aat	gca	ttt	gta	ttg	gaa	aat	aac	aat	aaa	ata	384
Asp	Leu	Leu	Phe	Phe	Asn	Ala	Phe	Val	Leu	Glu	Asn	Asn	Asn	Lys	Ile	
		115					120					125				
gaa	aga	aag	ttg	aat	ttt	caa	gaa	aaa	tgt	tat	gta	aaa	aaa	gat	ttt	432
Glu	Arg	Lys	Leu	Asn	Phe	Gln	Glu	Lys	Cys	Tyr	Val	Lys	Lys	Asp	Phe	
	130					135					140					
tta	aaa	gaa	cta	tta	aaa	act	aaa	aat	tta	ttt	tgg	aca	gtg	tgg	gca	480
Leu	Lys	Glu	Leu	Leu	Lys	Thr	Lys	Asn	Leu	Phe	Trp	Thr	Val	Trp	Ala	
145					150					155					160	



aaa gtc ata aaa aaa gaa tta tat ctc aag gct gtt ggt tta ata tcg	528
Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser	
165 170 175	
cta gaa aat gct aaa ata aat atg gct gaa gat gtt tta tta tat tac	576
Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr	
180 185 190	
cct ttg ata aat att tca aat act ata ttt cac ttg agt aaa aat tta	624
Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu	
195 200 205	
tac aat tat caa ata aat aat ttc tct ata acc aaa aca tta aca ttg	672
Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu	
210 215 220	
caa aat ata aaa aca aat ata caa gaa caa gat aat gtt cta tat ctt	720
Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu	
225 230 235 240	
cta aag aag atg caa tat aat tac aat ttt aac tta act ttg ctt aaa	768
Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys	
245 250 255	
tta att gag tat ttt tta tta att gaa aaa tac tca tta tca agc aag	816
Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys	
260 265 270	
cga aat gtt ctt tgt ttt aaa atc aat att ttt ttt aaa aaa atc caa	864
Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln	
275 280 285	
ttt aaa ttt tat cgc ttg ctg aag atg	891
Phe Lys Phe Tyr Arg Leu Leu Lys Met	
290 295	

<210> 31  
 <211> 297  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 31
Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
1 5 10 15
Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile
20 25 30
Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile
35 40 45
Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn
50 55 60
Glu Glu Asn Leu Lys Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
65 70 75 80
Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
85 90 95
Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile
100 105 110

Asp	Leu	Leu	Phe	Phe	Asn	Ala	Phe	Val	Leu	Glu	Asn	Asn	Asn	Lys	Ile
		115					120					125			
Glu	Arg	Lys	Leu	Asn	Phe	Gln	Glu	Lys	Cys	Tyr	Val	Lys	Lys	Asp	Phe
	130					135					140				
Leu	Lys	Glu	Leu	Leu	Lys	Thr	Lys	Asn	Leu	Phe	Trp	Thr	Val	Trp	Ala
145					150					155					160
Lys	Val	Ile	Lys	Lys	Glu	Leu	Tyr	Leu	Lys	Ala	Val	Gly	Leu	Ile	Ser
				165					170					175	
Leu	Glu	Asn	Ala	Lys	Ile	Asn	Met	Ala	Glu	Asp	Val	Leu	Leu	Tyr	Tyr
			180					185					190		
Pro	Leu	Ile	Asn	Ile	Ser	Asn	Thr	Ile	Phe	His	Leu	Ser	Lys	Asn	Leu
	195					200						205			
Tyr	Asn	Tyr	Gln	Ile	Asn	Asn	Phe	Ser	Ile	Thr	Lys	Thr	Leu	Thr	Leu
	210				215						220				
Gln	Asn	Ile	Lys	Thr	Asn	Ile	Gln	Glu	Gln	Asp	Asn	Val	Leu	Tyr	Leu
225					230					235					240
Leu	Lys	Lys	Met	Gln	Tyr	Asn	Tyr	Asn	Phe	Asn	Leu	Thr	Leu	Leu	Lys
			245						250					255	
Leu	Ile	Glu	Tyr	Phe	Leu	Leu	Ile	Glu	Lys	Tyr	Ser	Leu	Ser	Ser	Lys
		260						265					270		
Arg	Asn	Val	Leu	Cys	Phe	Lys	Ile	Asn	Ile	Phe	Phe	Lys	Lys	Ile	Gln
	275					280						285			
Phe	Lys	Phe	Tyr	Arg	Leu	Leu	Lys	Met							
	290					295									

<210> 32

<211> 295

<212> PRT

<213> Campylobacter jejuni

<220>

<223> lipid A biosynthesis acyltransferase from C.  
jejuni OH4384

<400> 32

Met	Lys	Asn	Ser	Asp	Arg	Ile	Tyr	Leu	Ser	Leu	Tyr	Tyr	Ile	Leu	Lys
1				5					10					15	
Phe	Phe	Val	Thr	Phe	Met	Pro	Asp	Cys	Ile	Leu	His	Phe	Leu	Ala	Leu
			20					25					30		
Ile	Val	Ala	Arg	Ile	Ala	Phe	His	Leu	Asn	Lys	Lys	His	Arg	Lys	Ile
	35					40						45			
Ile	Asn	Thr	Asn	Leu	Gln	Ile	Cys	Phe	Pro	Gln	Tyr	Thr	Gln	Lys	Glu
	50				55					60					
Arg	Asp	Lys	Leu	Ser	Leu	Lys	Ile	Tyr	Glu	Asn	Phe	Ala	Gln	Phe	Gly
65				70					75					80	
Ile	Asp	Cys	Leu	Gln	Asn	Gln	Asn	Thr	Thr	Lys	Glu	Lys	Ile	Leu	Asn
			85					90					95		
Lys	Val	Asn	Phe	Ile	Asn	Glu	Asn	Phe	Leu	Ile	Asp	Ala	Leu	Ala	Leu
		100					105						110		
Lys	Arg	Pro	Ile	Ile	Phe	Thr	Thr	Ala	His	Tyr	Gly	Asn	Trp	Glu	Ile
	115					120						125			
Leu	Ser	Leu	Ala	Tyr	Ala	Ala	Lys	Tyr	Gly	Ala	Ile	Ser	Ile	Val	Gly
130					135					140					
Lys	Lys	Leu	Lys	Ser	Glu	Val	Met	Tyr	Glu	Ile	Leu	Ser	Gln	Ser	Arg
145				150					155						160
Thr	Gln	Phe	Asp	Ile	Glu	Leu	Ile	Asp	Lys	Lys	Gly	Gly	Ile	Arg	Gln
			165					170					175		
Met	Leu	Ser	Ala	Leu	Lys	Lys	Glu	Arg	Ala	Leu	Gly	Ile	Leu	Thr	Asp
			180				185						190		

Gln	Asp	Cys	Val	Glu	Asn	Glu	Ser	Val	Arg	Leu	Lys	Phe	Phe	Asn	Lys
	195						200					205			
Glu	Val	Asn	Tyr	Gln	Met	Gly	Ala	Ser	Leu	Ile	Ala	Gln	Arg	Ser	Asn
	210					215					220				
Ala	Leu	Ile	Ile	Pro	Val	Tyr	Ala	Tyr	Lys	Glu	Gly	Gly	Lys	Phe	Cys
225					230					235					240
Ile	Glu	Phe	Phe	Lys	Ala	Lys	Asp	Ser	Gln	Asn	Ala	Ser	Leu	Glu	Glu
				245					250					255	
Leu	Thr	Leu	Tyr	Gln	Ala	Gln	Ser	Cys	Glu	Glu	Met	Ile	Lys	Lys	Arg
			260					265					270		
Pro	Trp	Glu	Tyr	Phe	Phe	Phe	His	Arg	Arg	Phe	Ala	Ser	Tyr	Asn	Glu
	275						280					285			
Glu	Ile	Tyr	Lys	Gly	Ala	Lys									
	290					295									

<210> 33  
 <211> 418  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> glycosyltransferase from C. jejuni OH4384 (ORF 3a  
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 33

Met	Asn	Leu	Lys	Gln	Ile	Ser	Val	Ile	Ile	Ile	Val	Lys	Asn	Ala	Glu
1				5				10						15	
Gln	Thr	Leu	Leu	Glu	Cys	Leu	Asn	Ser	Leu	Lys	Asp	Phe	Asp	Glu	Ile
		20						25					30		
Ile	Leu	Leu	Asn	Asn	Glu	Ser	Ser	Asp	Asn	Thr	Leu	Lys	Ile	Ala	Asn
		35					40					45			
Glu	Phe	Lys	Lys	Asp	Phe	Ala	Asn	Leu	Tyr	Ile	Tyr	His	Asn	Ala	Phe
	50					55					60				
Ile	Gly	Phe	Gly	Ala	Leu	Lys	Asn	Leu	Ala	Leu	Ser	Tyr	Ala	Lys	Asn
65					70				75						80
Asp	Trp	Ile	Leu	Ser	Ile	Asp	Ala	Asp	Glu	Val	Leu	Glu	Asn	Glu	Cys
			85						90					95	
Ile	Lys	Glu	Leu	Lys	Asn	Leu	Lys	Leu	Gln	Glu	Asp	Asn	Ile	Ile	Ala
		100						105					110		
Leu	Ser	Arg	Lys	Asn	Leu	Tyr	Lys	Gly	Glu	Trp	Ile	Lys	Ala	Cys	Gly
		115					120					125			
Trp	Trp	Pro	Asp	Tyr	Val	Leu	Arg	Ile	Phe	Asn	Lys	Asn	Phe	Thr	Arg
	130					135					140				
Phe	Asn	Asp	Asn	Leu	Val	His	Glu	Ser	Leu	Val	Leu	Pro	Ser	Asn	Ala
145					150				155						160
Lys	Lys	Ile	Tyr	Leu	Lys	Asn	Gly	Leu	Lys	His	Tyr	Ser	Tyr	Lys	Asp
				165					170					175	
Ile	Ser	His	Leu	Ile	Asp	Lys	Met	Gln	Tyr	Tyr	Ser	Ser	Leu	Trp	Ala
			180					185					190		
Lys	Gln	Asn	Ile	His	Lys	Lys	Ser	Gly	Val	Leu	Lys	Ala	Asn	Leu	Arg
		195					200					205			
Ala	Phe	Trp	Thr	Phe	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	Asn	Gly	Phe	Leu
	210					215					220				
Tyr	Gly	Tyr	Lys	Gly	Phe	Ile	Ile	Ser	Val	Cys	Ser	Ala	Leu	Gly	Thr
225					230					235					240
Phe	Phe	Lys	Tyr	Met	Lys	Leu	Tyr	Glu	Leu	Gln	Arg	Gln	Lys	Pro	Lys
				245					250					255	
Thr	Cys	Ala	Leu	Ile	Ile	Ile	Thr	Tyr	Asn	Gln	Lys	Glu	Arg	Leu	Lys
			260					265					270		

Leu Val Leu Asp Ser Val Lys Asn Leu Ala Phe Leu Pro Asn Glu Val  
           275                          280                          285  
 Leu Ile Ala Asp Asp Gly Ser Lys Glu Asp Thr Ala Arg Leu Ile Glu  
           290                          295                          300  
 Glu Tyr Gln Lys Asp Phe Pro Cys Pro Leu Lys His Ile Trp Gln Glu  
 305                          310                          315                          320  
 Asp Glu Gly Phe Lys Leu Ser Lys Ser Arg Asn Lys Thr Ile Lys Asn  
                           325                          330                          335  
 Ala Asp Ser Glu Tyr Ile Ile Val Ile Asp Gly Asp Met Ile Leu Glu  
                           340                          345                          350  
 Lys Asp Phe Ile Lys Glu His Leu Glu Phe Ala Gln Arg Lys Leu Phe  
           355                          360                          365  
 Leu Gln Gly Ser Arg Val Ile Leu Asn Lys Lys Glu Ser Glu Glu Ile  
           370                          375                          380  
 Leu Asn Lys Asp Asp Tyr Arg Ile Ile Phe Asn Lys Lys Asp Phe Lys  
 385                          390                          395                          400  
 Ser Ser Lys Asn Ser Phe Leu Ala Lys Ile Phe Tyr Ser Leu Ser Lys  
                           405                          410                          415  
 Lys Arg

<210> 34  
 <211> 389  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> glycosyltransferase of C. jejuni OH4384 (ORF 4a of  
       lipooligosaccharide (LOS) biosynthesis locus)

<400> 34  
 Met Lys Lys Ile Gly Val Val Ile Pro Ile Tyr Asn Val Glu Lys Tyr  
   1                          5                          10                          15  
 Leu Arg Glu Cys Leu Asp Ser Val Ile Asn Gln Thr Tyr Thr Asn Leu  
           20                          25                          30  
 Glu Ile Ile Leu Val Asn Asp Gly Ser Thr Asp Glu His Ser Leu Asn  
           35                          40                          45  
 Ile Ala Lys Glu Tyr Thr Leu Lys Asp Lys Arg Ile Thr Leu Phe Asp  
           50                          55                          60  
 Lys Lys Asn Gly Gly Leu Ser Ser Ala Arg Asn Ile Gly Ile Glu Tyr  
           65                          70                          75                          80  
 Phe Ser Gly Glu Tyr Lys Leu Lys Asn Lys Thr Gln His Ile Lys Glu  
                           85                          90                          95  
 Asn Ser Leu Ile Glu Phe Gln Leu Asp Gly Asn Asn Pro Tyr Asn Ile  
           100                          105                          110  
 Tyr Lys Ala Tyr Lys Ser Ser Gln Ala Phe Asn Asn Glu Lys Asp Leu  
           115                          120                          125  
 Thr Asn Phe Thr Tyr Pro Ser Ile Asp Tyr Ile Ile Phe Leu Asp Ser  
           130                          135                          140  
 Asp Asn Tyr Trp Lys Leu Asn Cys Ile Glu Glu Cys Val Ile Arg Met  
 145                          150                          155                          160  
 Lys Asn Val Asp Val Leu Trp Phe Asp His Asp Cys Thr Tyr Glu Asp  
                           165                          170                          175  
 Asn Ile Lys Asn Lys His Lys Lys Thr Arg Met Glu Ile Phe Asp Phe  
           180                          185                          190  
 Lys Lys Glu Cys Ile Ile Thr Pro Lys Glu Tyr Ala Asn Arg Ala Leu  
           195                          200                          205  
 Ser Val Gly Ser Arg Asp Ile Ser Phe Gly Trp Asn Gly Met Ile Asp  
           210                          215                          220  
 Phe Asn Phe Leu Lys Gln Ile Lys Leu Lys Phe Ile Asn Phe Ile Ile  
 225                          230                          235                          240

Asn Glu Asp Ile His Phe Gly Ile Ile Leu Phe Ala Ser Ala Asn Lys  
 245 250 255  
 Ile Tyr Val Leu Ser Gln Lys Leu Tyr Leu Cys Arg Leu Arg Ala Asn  
 260 265 270  
 Ser Ile Ser Asn His Asp Lys Lys Ile Thr Lys Ala Asn Val Ser Glu  
 275 280 285  
 Tyr Phe Lys Asp Ile Tyr Glu Thr Phe Gly Glu Asn Ala Lys Glu Ala  
 290 295 300  
 Lys Asn Tyr Leu Lys Ala Ala Ser Arg Val Ile Thr Ala Leu Lys Leu  
 305 310 315 320  
 Ile Glu Phe Phe Lys Asp Gln Lys Asn Glu Asn Ala Leu Ala Ile Lys  
 325 330 335  
 Glu Thr Phe Leu Pro Cys Tyr Ala Lys Lys Ala Leu Met Ile Lys Lys  
 340 345 350  
 Phe Lys Lys Asp Pro Leu Asn Leu Lys Glu Gln Leu Val Leu Ile Lys  
 355 360 365  
 Pro Phe Ile Gln Thr Lys Leu Pro Tyr Asp Ile Trp Lys Phe Trp Gln  
 370 375 380  
 Lys Ile Lys Asn Ile  
 385

<210> 35  
 <211> 346  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> sialic acid synthase from C. jejuni OH4384 (ORF 8a  
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 35  
 Met Lys Glu Ile Lys Ile Gln Asn Ile Ile Ile Ser Glu Glu Lys Ala  
 1 5 10 15  
 Pro Leu Val Val Pro Glu Ile Gly Ile Asn His Asn Gly Ser Leu Glu  
 20 25 30  
 Leu Ala Lys Ile Met Val Asp Ala Ala Phe Ser Thr Gly Ala Lys Ile  
 35 40 45  
 Ile Lys His Gln Thr His Ile Val Glu Asp Glu Met Ser Lys Ala Ala  
 50 55 60  
 Lys Lys Val Ile Pro Gly Asn Ala Lys Ile Ser Ile Tyr Glu Ile Met  
 65 70 75 80  
 Gln Lys Cys Ala Leu Asp Tyr Lys Asp Glu Leu Ala Leu Lys Glu Tyr  
 85 90 95  
 Thr Glu Lys Leu Gly Leu Val Tyr Leu Ser Thr Pro Phe Ser Arg Ala  
 100 105 110  
 Gly Ala Asn Arg Leu Glu Asp Met Gly Val Ser Ala Phe Lys Ile Gly  
 115 120 125  
 Ser Gly Glu Cys Asn Asn Tyr Pro Leu Ile Lys His Ile Ala Ala Phe  
 130 135 140  
 Lys Lys Pro Met Ile Val Ser Thr Gly Met Asn Ser Ile Glu Ser Ile  
 145 150 155 160  
 Lys Pro Thr Val Lys Ile Leu Leu Asp Asn Glu Ile Pro Phe Val Leu  
 165 170 175  
 Met His Thr Thr Asn Leu Tyr Pro Thr Pro His Asn Leu Val Arg Leu  
 180 185 190  
 Asn Ala Met Leu Glu Leu Lys Lys Glu Phe Ser Cys Met Val Gly Leu  
 195 200 205  
 Ser Asp His Thr Thr Asp Asn Leu Ala Cys Leu Gly Ala Val Ala Leu  
 210 215 220

Gly	Ala	Cys	Val	Leu	Glu	Arg	His	Phe	Thr	Asp	Ser	Met	His	Arg	Ser
225					230					235					240
Gly	Pro	Asp	Ile	Val	Cys	Ser	Met	Asp	Thr	Gln	Ala	Leu	Lys	Glu	Leu
				245					250					255	
Ile	Ile	Gln	Ser	Glu	Gln	Met	Ala	Ile	Met	Arg	Gly	Asn	Asn	Glu	Ser
			260					265					270		
Lys	Lys	Ala	Ala	Lys	Gln	Glu	Gln	Val	Thr	Ile	Asp	Phe	Ala	Phe	Ala
		275					280					285			
Ser	Val	Val	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Gly	Glu	Val	Leu	Ser	Met
	290					295					300				
Asp	Asn	Ile	Trp	Val	Lys	Arg	Pro	Gly	Leu	Gly	Gly	Ile	Ser	Ala	Ala
305					310					315					320
Glu	Phe	Glu	Asn	Ile	Leu	Gly	Lys	Lys	Ala	Leu	Arg	Asp	Ile	Glu	Asn
			325						330					335	
Asp	Thr	Gln	Leu	Ser	Tyr	Glu	Asp	Phe	Ala						
			340					345							

<210> 36  
 <211> 352  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> enzyme involved in sialic acid biosynthesis from  
 C. jejuni OH4384 (ORF 9a of lipooligosaccharide (LOS)  
 biosynthesis locus)

<400> 36

Met	Tyr	Arg	Val	Gln	Asn	Ser	Ser	Glu	Phe	Glu	Leu	Tyr	Ile	Phe	Ala
1				5					10					15	
Thr	Gly	Met	His	Leu	Ser	Lys	Asn	Phe	Gly	Tyr	Thr	Val	Lys	Glu	Leu
			20					25					30		
Tyr	Lys	Asn	Gly	Phe	Lys	Asn	Ile	Tyr	Glu	Phe	Ile	Asn	Tyr	Asp	Lys
		35				40						45			
Tyr	Phe	Ser	Thr	Asp	Lys	Ala	Leu	Ala	Thr	Thr	Ile	Asp	Gly	Phe	Ser
	50					55					60				
Arg	Tyr	Val	Asn	Glu	Leu	Lys	Pro	Asp	Leu	Ile	Val	Val	His	Gly	Asp
65				70						75				80	
Arg	Ile	Glu	Pro	Leu	Ala	Ala	Ala	Ile	Val	Gly	Ala	Leu	Asn	Asn	Ile
			85						90					95	
Leu	Val	Ala	His	Ile	Glu	Gly	Gly	Glu	Ile	Ser	Gly	Thr	Ile	Asp	Asp
			100					105					110		
Ser	Leu	Arg	His	Ala	Ile	Ser	Lys	Leu	Ala	His	Ile	His	Leu	Val	Asn
		115					120					125			
Asp	Glu	Phe	Ala	Lys	Arg	Arg	Leu	Met	Gln	Leu	Gly	Glu	Asp	Glu	Lys
	130					135					140				
Ser	Ile	Phe	Ile	Ile	Gly	Ser	Pro	Asp	Leu	Glu	Leu	Leu	Asn	Asp	Asn
145					150					155					160
Lys	Ile	Ser	Leu	Asn	Glu	Ala	Lys	Lys	Tyr	Tyr	Asp	Ile	Asn	Tyr	Glu
			165						170					175	
Asn	Tyr	Ala	Leu	Leu	Met	Phe	His	Pro	Val	Thr	Thr	Glu	Ile	Thr	Ser
		180						185					190		
Ile	Lys	Asn	Gln	Ala	Asp	Asn	Leu	Val	Lys	Ala	Leu	Ile	Gln	Ser	Asn
		195					200						205		
Lys	Asn	Tyr	Ile	Val	Ile	Tyr	Pro	Asn	Asn	Asp	Leu	Gly	Phe	Glu	Leu
	210					215					220				
Ile	Leu	Gln	Ser	Tyr	Glu	Glu	Leu	Lys	Asn	Asn	Pro	Arg	Phe	Lys	Leu
225					230					235					240
Phe	Pro	Ser	Leu	Arg	Phe	Glu	Tyr	Phe	Ile	Thr	Leu	Leu	Lys	Asn	Ala
			245						250					255	

Asp	Phe	Ile	Ile	Gly	Asn	Ser	Ser	Cys	Ile	Leu	Lys	Glu	Ala	Leu	Tyr
		260						265					270		
Leu	Lys	Thr	Ala	Gly	Ile	Leu	Val	Gly	Ser	Arg	Gln	Asn	Gly	Arg	Leu
		275					280					285			
Gly	Asn	Glu	Asn	Thr	Leu	Lys	Val	Asn	Ala	Asn	Ser	Asp	Glu	Ile	Leu
	290					295					300				
Lys	Ala	Ile	Asn	Thr	Ile	His	Lys	Lys	Gln	Asp	Leu	Phe	Ser	Ala	Lys
305					310					315					320
Leu	Glu	Ile	Leu	Asp	Ser	Ser	Lys	Leu	Phe	Phe	Glu	Tyr	Leu	Gln	Ser
			325						330					335	
Gly	Glu	Phe	Phe	Lys	Leu	Asn	Thr	Gln	Lys	Val	Phe	Lys	Asp	Ile	Lys
		340						345					350		

<210> 37  
 <211> 221  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> CMP-sialic acid synthetase from C. jejuni OH4384  
 (ORF 10a of lipooligosaccharide (LOS) biosynthesis  
 locus)

<400>	37														
Met	Ser	Leu	Ala	Ile	Ile	Pro	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Lys
1				5					10					15	
Asn	Lys	Asn	Leu	Val	Leu	Leu	Asn	Asn	Lys	Pro	Leu	Ile	Tyr	Tyr	Thr
		20					25						30		
Ile	Lys	Ala	Ala	Leu	Asn	Thr	Lys	Ser	Ile	Ser	Lys	Val	Val	Val	Ser
		35					40					45			
Ser	Asp	Ser	Asp	Glu	Ile	Leu	Asn	Tyr	Ala	Lys	Ser	Gln	Asn	Val	Asp
	50					55					60				
Ile	Leu	Lys	Arg	Pro	Ile	Ser	Leu	Ala	Gln	Asp	Asn	Thr	Thr	Ser	Asp
65				70						75				80	
Lys	Val	Leu	Leu	His	Ala	Leu	Lys	Phe	Tyr	Lys	Asp	Tyr	Glu	Asp	Val
			85					90						95	
Val	Phe	Leu	Gln	Pro	Thr	Ser	Pro	Leu	Arg	Thr	Asn	Ile	His	Ile	Asp
		100						105					110		
Glu	Ala	Phe	Asn	Leu	Tyr	Lys	Asn	Ser	Asn	Ala	Asn	Ala	Leu	Ile	Ser
		115				120						125			
Val	Ser	Glu	Cys	Asp	Asn	Lys	Ile	Leu	Lys	Ala	Phe	Val	Cys	Asn	Glu
	130					135					140				
Tyr	Gly	Asp	Leu	Ala	Gly	Ile	Cys	Asn	Asp	Glu	Tyr	Pro	Phe	Met	Pro
145				150					155					160	
Arg	Gln	Lys	Leu	Pro	Lys	Thr	Tyr	Met	Ser	Asn	Gly	Ala	Ile	Tyr	Ile
			165					170						175	
Leu	Lys	Ile	Lys	Glu	Phe	Leu	Asn	Asn	Pro	Ser	Phe	Leu	Gln	Ser	Lys
		180					185						190		
Thr	Lys	His	Phe	Leu	Met	Asp	Glu	Ser	Ser	Ser	Leu	Asp	Ile	Asp	Cys
		195				200						205			
Leu	Glu	Asp	Leu	Lys	Lys	Ala	Glu	Gln	Ile	Trp	Lys	Lys			
	210					215						220			

<210> 38  
 <211> 277  
 <212> PRT  
 <213> Campylobacter jejuni

<220>

<223> acetyltransferase from *C. jejuni* OH4384 (ORF 11a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 38

```
Met Glu Lys Ile Thr Leu Lys Cys Asn Lys Asn Ile Leu Asn Leu Leu
 1          5          10          15
Lys Gln Tyr Asn Ile Tyr Thr Lys Thr Tyr Ile Glu Asn Pro Arg Arg
          20          25          30
Phe Ser Arg Leu Lys Thr Lys Asp Phe Ile Thr Phe Pro Leu Glu Asn
          35          40          45
Asn Gln Leu Glu Ser Val Ala Gly Leu Gly Ile Glu Glu Tyr Cys Ala
          50          55          60
Phe Lys Phe Ser Asn Ile Leu His Glu Met Asp Ser Phe Ser Phe Ser
          65          70          75          80
Gly Ser Phe Leu Pro His Tyr Thr Lys Val Gly Arg Tyr Cys Ser Ile
          85          90          95
Ser Asp Gly Val Ser Met Phe Asn Phe Gln His Pro Met Asp Arg Ile
          100          105          110
Ser Thr Ala Ser Phe Thr Tyr Glu Thr Asn His Ser Phe Ile Asn Asp
          115          120          125
Ala Cys Gln Asn His Ile Asn Lys Thr Phe Pro Ile Val Asn His Asn
          130          135          140
Pro Ser Ser Ser Ile Thr His Leu Ile Ile Gln Asp Asp Val Trp Ile
          145          150          155          160
Gly Lys Asp Val Leu Leu Lys Gln Gly Ile Thr Leu Gly Thr Gly Cys
          165          170          175
Val Ile Gly Gln Arg Ala Val Val Thr Lys Asp Val Pro Pro Tyr Ala
          180          185          190
Ile Val Ala Gly Ile Pro Ala Lys Ile Ile Lys Tyr Arg Phe Asp Glu
          195          200          205
Lys Thr Ile Glu Arg Leu Leu Lys Ile Gln Trp Trp Lys Tyr His Phe
          210          215          220
Ala Asp Phe Tyr Asp Ile Asp Leu Asn Leu Lys Ile Asn Gln Tyr Leu
          225          230          235          240
Asp Leu Leu Glu Glu Lys Ile Ile Lys Lys Ser Ile Ser Tyr Tyr Asn
          245          250          255
Pro Asn Lys Leu Tyr Phe Arg Asp Ile Leu Glu Leu Lys Ser Lys Lys
          260          265          270
Ile Phe Asn Leu Phe
          275
```

<210> 39

<211> 270

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> glycosyltransferase from *C. jejuni* OH4384 (ORF 12a  
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 39

```
Met Pro Gln Leu Ser Ile Ile Ile Pro Leu Phe Asn Ser Cys Asp Phe
 1          5          10          15
Ile Ser Arg Ala Leu Gln Ser Cys Ile Asn Gln Thr Leu Lys Asp Ile
          20          25          30
Glu Ile Leu Ile Ile Asp Asp Lys Ser Lys Asp Asn Ser Leu Asn Met
          35          40          45
Val Leu Glu Phe Ala Lys Lys Asp Pro Arg Ile Lys Ile Phe Gln Asn
          50          55          60
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Glu	Glu	Asn	Leu	Gly	Thr	Phe	Ala	Ser	Arg	Asn	Leu	Gly	Val	Leu	His
65					70					75					80
Ser	Ser	Ser	Asp	Phe	Ile	Met	Phe	Leu	Asp	Ser	Asp	Asp	Phe	Leu	Thr
				85					90					95	
Pro	Asp	Ala	Cys	Glu	Ile	Ala	Phe	Lys	Glu	Met	Lys	Lys	Gly	Phe	Asp
			100					105					110		
Leu	Leu	Cys	Phe	Asp	Ala	Phe	Val	His	Arg	Val	Lys	Thr	Lys	Gln	Phe
		115					120					125			
Tyr	Arg	Phe	Lys	Gln	Asp	Glu	Val	Phe	Asn	Gln	Lys	Glu	Phe	Leu	Glu
	130					135					140				
Phe	Leu	Ser	Lys	Gln	Arg	His	Phe	Cys	Trp	Ser	Val	Trp	Ala	Lys	Cys
145				150						155					160
Phe	Lys	Lys	Asp	Ile	Ile	Leu	Lys	Ser	Phe	Glu	Lys	Ile	Lys	Ile	Asp
			165					170						175	
Glu	Arg	Leu	Asn	Tyr	Gly	Glu	Asp	Val	Leu	Phe	Cys	Tyr	Ile	Tyr	Phe
			180					185					190		
Met	Phe	Cys	Glu	Lys	Ile	Ala	Val	Phe	Lys	Thr	Cys	Ile	Tyr	His	Tyr
		195					200					205			
Glu	Phe	Asn	Pro	Asn	Gly	Arg	Tyr	Glu	Asn	Lys	Asn	Lys	Glu	Ile	Leu
	210					215					220				
Asn	Gln	Asn	Tyr	His	Asp	Lys	Lys	Lys	Ser	Asn	Glu	Ile	Ile	Lys	Lys
225				230						235					240
Leu	Ser	Lys	Glu	Phe	Ala	His	Asp	Glu	Phe	His	Gln	Lys	Leu	Phe	Glu
				245				250						255	
Val	Leu	Lys	Arg	Glu	Glu	Ala	Gly	Val	Lys	Asn	Arg	Leu	Lys		
			260					265					270		

<210> 40  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ42 primer in  
 heptosyltransferase-II used to amplify LPS core  
 biosynthesis locus

<400> 40  
 gccattaccg tatcgcttaa ccagg

25

<210> 41  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ43 primer in  
 heptosyltransferase-I used to amplify LPS core  
 biosynthesis locus

<400> 41  
 aaagaatacg aatttgctaa agagg

25

<210> 42  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-106 3'  
 primer used to amplify and clone ORF 5a

<400> 42  
 cctagggtcga cttaaaacaa tgtaagaat atttttttta g 41

<210> 43  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-157 5'  
 primer used to amplify and clone ORF 5a

<400> 43  
 cttaggaggt catatgctat ttcaatcata ctttgtg 37

<210> 44  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-105 3'  
 primer used to amplify and clone ORF 6a

<400> 44  
 cctagggtcga cctctaaaaa aaatattctt aacattg 37

<210> 45  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-133 5'  
 primer used to amplify and clone ORF 6a

<400> 45  
 cttaggaggt catatgttta aaatttcaat catcttacc 39

<210> 46  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-131 5'  
 primer used to amplify and clone ORF 7a

<400> 46  
 cttaggaggt catatgaaaa aagttattat tgctggaaat g 41

<210> 47  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CJ-132 3'  
 primer used to amplify and clone ORF 7a

<400> 47  
 cctaggtcga cttattttcc ttgaaataa tgctttatat c

41

<210> 48  
 <211> 322  
 <212> PRT  
 <213> Campylobacter jejuni

<220>  
 <223> Campylobacter alpha-2,3-sialyltransferase I (Cst-I)  
 from C. jejuni OH4384

<400> 48  
 Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met  
           1                  5                  10                  15  
 Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn  
                   20                  25                  30  
 Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe  
           35                  40                  45  
 Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe  
           50                  55                  60  
 Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu  
           65                  70                  75                  80  
 Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe  
                   85                  90                  95  
 Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn  
                   100                  105                  110  
 Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys  
           115                  120                  125  
 Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg  
           130                  135                  140  
 Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr  
           145                  150                  155                  160  
 Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile  
                   165                  170                  175  
 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly  
           180                  185                  190  
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile  
           195                  200                  205  
 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala  
           210                  215                  220  
 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn  
           225                  230                  235                  240  
 Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn  
                   245                  250                  255  
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn  
           260                  265                  270  
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu  
           275                  280                  285  
 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val  
           290                  295                  300

Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His  
 305 310 315 320  
 Leu Ser

<210> 49  
 <211> 231  
 <212> PRT  
 <213> Haemophilus influenzae

<220>  
 <223> putative ORF from GenBank #U32720

<400> 49  
 Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu  
 1 5 10 15  
 Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn  
 20 25 30  
 Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn  
 35 40 45  
 Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu  
 50 55 60  
 Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val  
 65 70 75 80  
 Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu  
 85 90 95  
 Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys  
 100 105 110  
 Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser  
 115 120 125  
 Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly  
 130 135 140  
 Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe  
 145 150 155 160  
 Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys  
 165 170 175  
 Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys  
 180 185 190  
 Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe  
 195 200 205  
 Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala  
 210 215 220  
 Leu Lys Ser Arg Lys Trp Asp  
 225 230